

Serial Number: 07/371, 333A

ENTERED



Changed a file from non-ASCII to ASCII



Changed the margins in cases where the sequence text was "wrapped" down to the next line.



Edited a format error in the Current Application Data section, specifically:

Edited the Current Application Data section with the actual current number. The number inputted by the applicant was ☐ the prior application data; or ☐ other

Added the mandatory heading and subheadings for "Current Application Data".



Edited the "Number of Sequences" field. The applicant spelled out a number instead of using an integer.



Changed the spelling of a mandatory field (the headings or subheadings), specifically:



Corrected the SEQ ID NO when obviously incorrect. The sequence numbers that were edited were:



Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited:



Corrected subheading placement. All responses must be on the same line as each subheading. If the applicant placed a response below the subheading, this was moved to its appropriate place.



Inserted colons after headings/subheadings. Headings edited included:



Deleted extra, invalid, headings used by an applicant, specifically:

Deleted: ☒ non-ASCII "garbage" at the beginning/end of files; ☐ secretary initials/filename at end of file; ☐ page numbers throughout text; ☐ other invalid text, such as

Inserted mandatory headings, specifically:



Corrected an obvious error in the response, specifically:



Edited identifiers where upper case is used but lower case is required, or vice versa.



Corrected an error in the Number of Sequences field, specifically:



A "Hard Page Break" code was inserted by the applicant. All occurrences had to be deleted.

Deleted *ending* stop codon in amino acid sequences and adjusted the "(A)Length:" field accordingly (error due to a PatentIn bug). Sequences corrected:

Other:

*Examiner: The above corrections must be communicated to the applicant in the first Office Action. DO NOT send a copy of this form.

3/1/95

1646

RAW SEQUENCE LISTING DATE: 03/05/2001
 PATENT APPLICATION: US/09/371,333A TIME: 14:42:25

Input Set : A:\Pto.vsk
 Output Set: N:\CRF3\03052001\I371333A.raw

```

3 <110> APPLICANT: Xu, Wenfeng
4   Presnell, Scott R.
5   Yee, David P.
6   Foster, Donald C.
8 <120> TITLE OF INVENTION: PROTEASE-ACTIVATED RECEPTOR PARA
9   (ZCHEMR2)
11 <130> FILE REFERENCE: 98-10D1
13 <140> CURRENT APPLICATION NUMBER: US 09/371,333A
14 <141> CURRENT FILING DATE: 1999-08-10
16 <150> PRIOR APPLICATION NUMBER: US 09/053,866
17 <151> PRIOR FILING DATE: 1998-04-01
19 <160> NUMBER OF SEQ ID NOS: 21
21 <170> SOFTWARE: FastSEQ for Windows Version 3.0
23 <210> SEQ ID NO: 1
24 <211> LENGTH: 4895
25 <212> TYPE: DNA
26 <213> ORGANISM: Homo sapiens
28 <220> FEATURE:
29 <221> NAME/KEY: CDS
30 <222> LOCATION: (176)...(1330)
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35   ggtccggcga ggcaggaagc ctgaggccac agcccagagc agcctgagtg cagtc atg   178
36                                     Met
37                                     1
39   tgg ggg cga ctg ctc ctg tgg ccc ctg gty ctg ggg ttc agc ctg tct   226
40   Trp Gly Arg Leu Leu Leu Trp Pro Leu Val Leu Gly Phe Ser Leu Ser
41       5                10                15
43   ggc ggc acc cag acc ccc agc gtc tac gac gag agc ggg agc acc gga   274
44   Gly Gly Thr Gln Thr Pro Ser Val Tyr Asp Glu Ser Gly Ser Thr Gly
45       20                25                30
47   ggt ggt gat gac agc acg ccc tca atc ctg cct gcc ccc cgc ggc tac   322
48   Gly Gly Asp Asp Ser Thr Pro Ser Ile Leu Pro Ala Pro Arg Gly Tyr
49       35                40                45
51   cca ggc caa gtc tgt gcc aat gac agt gac acc ctg gag ctc ccg gac   370
52   Pro Gly Gln Val Cys Ala Asn Asp Ser Asp Thr Leu Glu Leu Pro Asp
53       50                55                60                65
55   agc tca cgg gca ctg ctt ctg ggc tgg gty ccc acc agg ctg gty ccc   418
56   Ser Ser Arg Ala Leu Leu Gly Trp Val Pro Thr Arg Leu Val Pro
57       70                75                80
59   gcc ctc tat ggg ctg gtc ctg gty gty ggg ctg ccg gcc aat ggg ctg   466
60   Ala Leu Tyr Gly Leu Val Leu Val Val Gly Leu Pro Ala Asn Gly Leu
61       85                90                95
63   gcg ctg tgg gty ctg gcc acg cag gca cct cgg ctg ccc tcc acc atg   514
64   Ala Leu Trp Val Leu Ala Thr Gln Ala Pro Arg Leu Pro Ser Thr Met
65       100               105               110

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Input Set : A:\Pto.vsk

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67	ctg ctg atg aac ctc gcg act gct gac ctc ctg ctg gcc ctg gcg ctg	562
68	Leu Leu Met Asn Leu Ala Thr Ala Asp Leu Leu Leu Ala Leu Ala Leu	
69	115 120 125	
71	ccc ccg cgg atc gcc tac cac ctg cgt ggc cag cgc tgg ccc ttc ggg	610
72	Pro Pro Arg Ile Ala Tyr His Leu Arg Gly Gln Arg Trp Pro Phe Gly	
73	130 135 140 145	
75	gag gcc gcc tgc cgc ctg gcc acg gcc gca ctc tat ggt cac atg tat	658
76	Glu Ala Ala Cys Arg Leu Ala Thr Ala Ala Leu Tyr Gly His Met Tyr	
77	150 155 160	
79	ggc tca gtg ctg ctg ctg gcc gcc gtc agc ctg gat cgc tac ctg gcc	706
80	Gly Ser Val Leu Leu Leu Ala Ala Val Ser Leu Asp Arg Tyr Leu Ala	
81	165 170 175	
83	ctg gtg cac ccg ctg cgg gcc cgc gcc ctg cgt ggc cgg cgc ctg gcc	754
84	Leu Val His Pro Leu Arg Ala Arg Ala Leu Arg Gly Arg Arg Leu Ala	
85	180 185 190	
87	ctt gga ctc tgc atg gct gct tgg ctc atg gcg gcc gcc ctg gca ctg	802
88	Leu Gly Leu Cys Met Ala Ala Trp Leu Met Ala Ala Ala Leu Ala Leu	
89	195 200 205	
91	ccc ctg aca ctg cag cgg cag acc ttc cgg ctg gcg cgc tcc gat cgc	850
92	Pro Leu Thr Leu Gln Arg Gln Thr Phe Arg Leu Ala Arg Ser Asp Arg	
93	210 215 220 225	
95	gtg ctc tgc cat gac gcg ctg ccc ctg gac gca cag gcc tcc cac tgg	898
96	Val Leu Cys His Asp Ala Leu Pro Leu Asp Ala Gln Ala Ser His Trp	
97	230 235 240	
99	caa ccg gcc ttc acc tgc ctg gcg ctg ttg ggc tgt ttc ctg ccc ctg	946
100	Gln Pro Ala Phe Thr Cys Leu Ala Leu Leu Gly Cys Phe Leu Pro Leu	
101	245 250 255	
103	ctg gcc atg ctg ctg tgc tac ggg gcc acc ctg cac acg ctg gcg gcc	994
104	Leu Ala Met Leu Leu Cys Tyr Gly Ala Thr Leu His Thr Leu Ala Ala	
105	260 265 270	
106	agc ggc cgg cgc tac ggc cac gcg ctg agg ctg acc gca gtg gtg ctg	1042
107	Ser Gly Arg Arg Tyr Gly His Ala Leu Arg Leu Thr Ala Val Val Leu	
108	275 280 285	
110	gcc tcc gcc gtg gcc ttc ttc gtg ccc agc aac ctg ctg ctg ctg ctg	1090
111	Ala Ser Ala Val Ala Phe Phe Val Pro Ser Asn Leu Leu Leu Leu Leu	
112	290 295 300 305	
114	cat tac tcg gac ccg agc ccc agc gcc tgg ggc aac ctc tat ggt gcc	1138
115	His Tyr Ser Asp Pro Ser Pro Ser Ala Trp Gly Asn Leu Tyr Gly Ala	
116	310 315 320	
118	tac gtg ccc agc ctg gcg ctg agc acc ctc aac agc tgc gtg gat ccc	1186
119	Tyr Val Pro Ser Leu Ala Leu Ser Thr Leu Asn Ser Cys Val Asp Pro	
120	325 330 335	
122	ttc atc tac tac tac gtg tcg gcc gag ttc agg gac aag gtg cgg gca	1234
123	Phe Ile Tyr Tyr Tyr Val Ser Ala Glu Phe Arg Asp Lys Val Arg Ala	
124	340 345 350	
126	ggg ctc ttc caa cgg tcg ccg ggg gac acc gtg gcc tcc aag gcc tct	1282
127	Gly Leu Phe Gln Arg Ser Pro Gly Asp Thr Val Ala Ser Lys Ala Ser	
128	355 360 365	
130	gcg gaa ggg ggc agc cgg ggc atg ggc acc cac tcc tct ttg ctc cag	1330

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131	Ala	Glu	Gly	Gly	Ser	Arg	Gly	Met	Gly	Thr	His	Ser	Ser	Leu	Leu	Gln	/
132	370				375				380					385			
134	tgacacaaag	tygggaaggc	tgtactgggt	cgaacagggt	cccttcccc	acttcacgtc											1390
135	cttcctggga	cctcagaatg	tgaccttatt	tgaaaatagg	gttggtacaa	ctgtcactag											1450
136	cggaggtcac	tttgagaag	ggtgggctt	acatccagt	tggtggtgt	cctcataaga											1510
137	taagygaggg	ccaggcctgg	tggtcacgc	ctgtaatccc	agcacttta	gaggccaagg											1570
138	cggatggatc	acttgagccc	aggagttcaa	caccagctg	agcaacatgg	laaaaccca											1630
139	tctctaccaa	aaatacaaaa	attagctggg	cttggtggct	ggcgctgta	atcccagcta											1690
140	ctcaggagac	tgaggcagaa	ggatcgcttg	aacctgggag	gcagaggttg	cagtgcgcg											1750
141	agattgccc	actggactcc	agcctgcgtg	acagagagcc	tgtctctaaa	tttaattaatt											1810
142	aaltaattta	attcaatttt	aaaaagacga	aaagtyacgg	ccaggtgcag	tggtcacgc											1870
143	ctataatctc	agcaactctg	gaggccaaga	tgaggattg	cttgaagcca	ggagtttggg											1930
144	accagcctgg	gcaacatagg	gggatcccat	ctctacacac	aaaaaatttt	tttaatgaac											1990
145	caggcattgt	ggcatgcgcc	tatagtccca	gccactcaag	aggcacaggg	gggaggatca											2050
146	cttgagccctg	ggaggttgg	gttgacgtga	gctatgattg	taccactgca	ctccagcctg											2110
147	ggcaacagag	caagaccttg	tctcaaaaat	aaacaaacta	aaattaaaaa	aagaagacga											2170
148	gagatagtgg	gtytggtggc	tcacacctgc	aatcccagca	ctttggaagg	ccgaggtggg											2230
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150	taccaaaaat	acaaaaatta	gccaggcgtg	gtggtgggca	cctgtactgg	ggaggtgccc											2350
151	accagctac	tggggagggt	gagtcaggag	aatcgcttga	acctgggagg	cggaggttgc											2410
152	ggtcagctga	gatggtgcca	ctgcactcca	gctgggcga	aagagcgact	ctgtctccaa											2470
153	aaaaaagaga	agaggagagg	acacagagac	acacagagaa	gaaagccatg	tggcggcaga											2530
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155	gccaacagcc	accagcagcc	aggagacagg	cctgggacgg	gctctcctc	acagcctcca											2650
156	gagggaaacca	gccctgccac	caccttgacc	ctggacttct	ggcctgcaga	actgtgagac											2710
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179	agtagtctga	cacggagact	ggcagcgccg	acgtcctgcc	caccacgcac	tcctggagag											4090
180	cacggaaccg	cacgcacgtc	aggcaccggc	tggggatctg	tggggcaggc	gcgggcycag											4150

TECH CENTER 1600/2900

MAR 0 8 2001

RECEIVED

RAW SEQUENCE LISTING DATE: 03/05/2001
 PATENT APPLICATION: US/09/371,333A TIME: 14:42:25

Input Set : A:\Pto.vsk
 Output Set: N:\CRF3\03052001\I371333A.raw

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181 gctcgaccg ggccaggagg cccggggcgc tgagctcagg ccagaaactg gctgatttca 4210
182 gggataccca ggacgcgtga aacacagaag aaacgtgac ccattttctt tttttctttt 4270
183 acttttcttt tttttttttt ttcctgagac agagtctcgc gctgttgccc aggctggagt 4330
184 gcagtggcgt gatctcggct cactgraagc tcggcctcct gggttcaaat gattctcctg 4390
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186 gtatttttga tcaagacgga gtttcacat gttggccagg ctggtctcca actcctgccc 4510
187 tcaagtgate cgctcgggtc ccatttttta ttctttgggt cctccatccc cactgggaaa 4570
188 acgtctcagg tggcctctga aacaccactc ctttttgtgt gtgtgcacgc atggctgagc 4630
189 atgtgtgggt gggagtcaag acattcacga tactgtgcaa tcatcacctc tgtctagtta 4690
190 caggacggtt tctttctccc ccuaagaaac cccatcgcca tcagcactca ctccccactc 4750
191 cccagcccc tggcaaccac aaatctttcc aactctacgg atttgctgt tctgggcatt 4810
192 tcatgtcaat ggaatcatgt actctgtgaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 4870
193 aaaaaaaaaa aaaaaaaaaa aaaaaa 4895
195 <210> SEQ ID NO: 2
196 <211> LENGTH: 385
197 <212> TYPE: PRT
198 <213> ORGANISM: Homo sapiens
200 <400> SEQUENCE: 2
201 Met Trp Gly Arg Leu Leu Trp Pro Leu Val Leu Gly Phe Ser Leu
202 1 5 10 15
203 Ser Gly Gly Thr Gln Thr Pro Ser Val Tyr Asp Glu Ser Gly Ser Thr
204 20 25 30
206 Gly Gly Gly Asp Asp Ser Thr Pro Ser Ile Leu Pro Ala Pro Arg Gly
207 35 40 45
208 Tyr Pro Gly Gln Val Cys Ala Asn Asp Ser Asp Thr Leu Glu Leu Pro
209 50 55 60
210 Asp Ser Ser Arg Ala Leu Leu Leu Gly Trp Val Pro Thr Arg Leu Val
211 65 70 75 80
212 Pro Ala Leu Tyr Gly Leu Val Leu Val Val Gly Leu Pro Ala Asn Gly
213 85 90 95
214 Leu Ala Leu Trp Val Leu Ala Thr Gln Ala Pro Arg Leu Pro Ser Thr
215 100 105 110
216 Met Leu Leu Met Asn Leu Ala Thr Ala Asp Leu Leu Leu Ala Leu Ala
217 115 120 125
218 Leu Pro Pro Arg Ile Ala Tyr His Leu Arg Gly Gln Arg Trp Pro Phe
219 130 135 140
220 Gly Glu Ala Ala Cys Arg Leu Ala Thr Ala Ala Leu Tyr Gly His Met
221 145 150 155 160
222 Tyr Gly Ser Val Leu Leu Ala Ala Val Ser Leu Asp Arg Tyr Leu
223 165 170 175
224 Ala Leu Val His Pro Leu Arg Ala Arg Ala Leu Arg Gly Arg Arg Leu
225 180 185 190
226 Ala Leu Gly Leu Cys Met Ala Ala Trp Leu Met Ala Ala Ala Leu Ala
227 195 200 205
228 Leu Pro Leu Thr Leu Gln Arg Gln Thr Phe Arg Leu Ala Arg Ser Asp
229 210 215 220
230 Arg Val Leu Cys His Asp Ala Leu Pro Leu Asp Ala Gln Ala Ser His
231 225 230 235 240
232 Trp Gln Pro Ala Phe Thr Cys Leu Ala Leu Leu Gly Cys Phe Leu Pro

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233           245           250           255
234 Leu Leu Ala Met Leu Leu Cys Tyr Gly Ala Thr Leu His Thr Leu Ala
235           260           265           270
236 Ala Ser Gly Arg Arg Tyr Gly His Ala Leu Arg Leu Thr Ala Val Val
237           275           280           285
238 Leu Ala Ser Ala Val Ala Phe Phe Val Pro Ser Asn Leu Leu Leu Leu
239           290           295           300
240 Leu His Tyr Ser Asp Pro Ser Pro Ser Ala Trp Gly Asn Leu Tyr Gly
241           305           310           315           320
242 Ala Tyr Val Pro Ser Leu Ala Leu Ser Thr Leu Asn Ser Cys Val Asp
243           325           330           335
244 Pro Phe Ile Tyr Tyr Tyr Val Ser Ala Glu Phe Arg Asp Lys Val Arg
245           340           345           350
246 Ala Gly Leu Phe Gln Arg Ser Pro Gly Asp Thr Val Ala Ser Lys Ala
247           355           360           365
248 Ser Ala Glu Gly Gly Ser Arg Gly Met Gly Thr His Ser Ser Leu Leu
249           370           375           380
250 Gln
251 385

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253 <210> SEQ ID NO: 3
254 <211> LENGTH: 1155
255 <212> TYPE: DNA
256 <213> ORGANISM: Artificial Sequence
258 <220> FEATURE:
259 <223> OTHER INFORMATION: This degenerate nucleotide sequence encodes the
260 amino acid sequence of SEQ ID NO:2.
262 <221> NAME/KEY: variation
263 <222> LOCATION: (1)...(1155) /
264 <223> OTHER INFORMATION: N is any nucleotide.
266 <400> SEQUENCE: 3

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W--> 268 caracnccnw sngntayga ygarwsnggn wsnaacngng gngngayga ywsnacnccn 120
W--> 269 wsnathytn cngcncnmng nggntayccn ggncargtnt gygcnaayga ywsngayacn 180
W--> 270 ytngarytn cngaywsnws nmngncnytn ytnytnngnt gggtnccnac nmgnytngt 240
W--> 271 ccngcnytn ayggnytngt nytnngntgn ggnytnccng cnaayggnyt ngcnytngtg 300
W--> 272 gtnytnacna cncargcncc nmgnytnccn wsnaacnatg tnytnatgaa yytnacnacn 360
W--> 273 gcngayytny tnytnacnytn ngcnytnccn ccmgnathg cntaycayyt nmngngncar 420
W--> 274 mgntggccnt tyggngargc ngcntgymgn ytnacnacng cngcnytna yggncaytg 480
W--> 275 tayggwnsng tnytnytnyt ngcngcngtn wsnytnngaym gntayytngc nytngtncay 540
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W--> 277 tggynatgng cngcngcnytn ngcnytnccn ytnacnytn armgncarac nttymgnytn 660
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W--> 279 tggcargcng cnttyacntg yytnacnytn ytnngntgyt tytnccnytn nytnacnatg 780
W--> 280 ytnytnngyt ayggngcnac nytnacayacn ytnacngcnw snggnmgngm ntayggncay 840
W--> 281 gcnynmgny tnaacngcngt ngtnytnngcn wngcngtng cnttytygt nccnwsnaay 900
W--> 282 ytnytnytny tnytnayta ywsngayccn wsncnwsng cntggggnaa yytnayggn 960
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W--> 284 taytaygtw sngcngartt ymgngayaar gtnmgngcng gnytnntyca rmgnwsnccn 1080
W--> 285 ggngayacng tngcnwsnaa rgcwnsngcn gargnggnw sngngngnat gggnacncay 1140

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VERIFICATION SUMMARY DATE: 03/05/2001
PATENT APPLICATION: US/09/371,333A TIME: 14:42:26

Input Set : A:\Pto.vsk
Output Set: N:\CRF3\03052001\I371333A.raw

L:267 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:268 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:269 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:270 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:271 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:272 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:273 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:274 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:275 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:276 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
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L:278 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:279 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
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L:281 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:282 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:283 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:284 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:285 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:286 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3